SEQUENCE LISTING

- <110> MASTROIANNI, NADIA CAINARCA, SILVIA CORAZZA, SABRINA
- <120> PHOTOPROTEINS WITH ENHANCED BIOLUMINESCENCE AND ASSAYS USING THE SAME
- <130> 100506-00028
- <140> 10/587,523
- <141> 2006-03-09
- <150> 05005390.9
- <151> 2005-11-03
- <150> 06000171.6
- <151> 2006-05-01
- <160> 24
- <170> PatentIn Ver. 3.3
- <210> 1
- <211> 198
- <212> PRT
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- Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys 35 40 45
- Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr 50
- Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met 65 70 75 80
- Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser
- Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp 115 120 125
- Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile 130 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His 145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg 165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu 180 185 190

Tyr Gly Asn Phe Val Pro 195

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Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu 20 25 30

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys 35 40 45

Ala Ser Asp Asp Ile Ser Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr 50 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met 65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser 100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp 115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile 130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg 165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu 180 185 190 Tyr Gly Asn Phe Val Pro 195

<210> 3

<211> 198

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 protein construct

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Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr 50 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met 65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys \$85\$ 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser 100 105 . 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp 115 120 125

Gly Ser Gly Cys Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile 130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His 145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg 165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu 180 185 190

Tyr Gly Asn Phe Val Pro 195

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<210> 4
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<211> 198

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Arg 35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr 50 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys.Ile Gly Met 65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser 100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp 115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile 130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His 145 150 150 155

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg 165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu 180 185 190

Tyr Gly Asp Phe Val Pro 195

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<211> 198

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
 protein construct

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Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu 20 25 . 30

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys 35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr 50 60

Lys Arg His Arg Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met 65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Val Phe Val Asp Gly Trp Lys
85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser 100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp 115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile 130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His 145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg 165 170 175

Gln His Leu Gly Phe Trp Tyr Ile Leu Asp Pro Asn Ala Asp Gly Leu 180 185 190

Tyr Gly Asn Phe Val Pro 195

<210> 6

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic protein construct

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1 5 10 15

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Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr 50 $\,$ 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met 65 70 75 80

Asp Phe Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys 85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Asn Lys Ser 100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Leu Asp Lys Asp 115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile 130 140

Ser Gly Ile Cys Arg Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His 145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg 165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu 180 185 190

Tyr Cly Asn Phe Val Pro 195

<210> 7 <211> 198

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein construct

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Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu 20 25 30

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys 35 40

Ala Ser Asp Asp Ile Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr 50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys 85 90 95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser 100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp 115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Cys Arg Ile 130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His 145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg 165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu 180 185 190

Tyr Gly Asn Phe Val Pro 195

<210> 8

<211> 198

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic protein construct

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Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu 20 25 30

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys 35 40 45

Ala Ser Asp Asp Val Cys Ala Lys Leu Gly Ala Thr Pro Glu Gln Thr 50 55 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met 65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser 100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp 115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile 130 \$135\$

Ser Gly Ile Cys Arg Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His 145 150 155 160

Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg 165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu 180 185 190

Tyr Gly Asn Phe Val Pro 195

<210> 9

<211> 198

<212> PRT

<213> Artificial Sequence

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 protein construct

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Asp Asp Pro Lys Trp Val Asn Arg Hib Lys Phe Met Phe Asn Phe Leu 20 25 30

Asp Ile Asn Gly Asp Gly Lys Val Thr Leu Asp Glu Ile Val Ser Lys 35 45

Ala Ser Asp Asp Ile Cys Ala Arg Leu Gly Ala Thr Pro Glu Gln Thr 50 60

Lys Arg His Gln Asp Ala Val Glu Ala Phe Phe Lys Lys Ile Gly Met
65 70 75 80

Asp Tyr Gly Lys Glu Val Glu Phe Pro Ala Phe Val Asp Gly Trp Lys
85
90
95

Glu Leu Ala Asn Tyr Asp Leu Lys Leu Trp Ser Gln Asn Lys Lys Ser 100 105 110

Leu Ile Arg Asp Trp Gly Glu Ala Val Phe Asp Ile Phe Asp Lys Asp
115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile 130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His 145 150 155 160 Cys Asp Leu Asp Asn Ser Gly Lys Leu Asp Val Asp Glu Met Thr Arg 165 170 175

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu 180 \$185\$

Tyr Gly Asn Phe Val Pro 195

<210> 10

<211> 198

<212> PRT

<213> Artificial Sequence

-220-

<223> Description of Artificial Sequence: Synthetic protein construct

<400> 10

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Asp Asn Pro Lys Trp Val Asn Arg His Lys Phe Met Phe Asn Phe Leu 20 25 30

Asp Ile Asn Gly Asp Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys 35 40 45

Ala Ser Asp Asp Ile Cys Ala Lys Leu Glu Ala Thr Pro Glu Gln Thr
50 60

Lys Arg His Gln Val Cys Val Glu Ala Phe Phe Arg Gly Cys Gly Met 65 70 75 80

Glu Tyr Gly Lys Glu Ile Ala Phe Pro Gln Phe Leu Asp Gly Trp Lys 85 90 95

Gln Leu Ala Thr Ser Glu Leu Lys Lys Trp Ala Arg Asn Glu Pro Thr $$^{\circ}$$ 100 \$105\$ 110

Leu Ile Arg Glu Trp Gly Asp Ala Val Phe Asp Ile Phe Asp Lys Asp 115 120 125

Gly Ser Gly Ser Ile Ser Leu Asp Glu Trp Lys Ala Tyr Gly Arg Ile 130 135 140

Ser Gly Ile Cys Ser Ser Asp Glu Asp Ala Glu Lys Thr Phe Lys His 145 150 155 160

Gln His Leu Gly Phe Trp Tyr Thr Leu Asp Pro Asn Ala Asp Gly Leu 180 185 190

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Tyr Gly Asn Phe Val Pro
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accetggacg agategtgag caaggecage gacgacatet gegecaaget gggegecace 180
cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240
gactacggca aggaggtgga gttccccgcc ttcgtggacg gctggaagga gctggccaac 300
taccacctga agctgtggag ccagaacaag aagagcctca tcagggactg gggcgaggcc 360
gtgttcgaca tcttcgacaa ggacggcagc ggctgcatca gcctggatga gtggaaggcc 420
tacggcagaa tcagcggcat ctgcagcagc gacgaggacg ccgaaaagac cttcaagcac 480
tqcqacctgq acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctggac 540
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<210> 12
<211> 600
<212> DNA
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<220>
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accetggacg agategtgag caaggecage gacgacatet gegecaaget gggegecaee 180
cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240
gactacggca aggaggtgga gttccccgcc ttcgtggacg gctggaagga gctggccaac 300
tacgacetga agetgtggag ecagaacaag aagageetea teagggaetg gggegaggee 360
gtgttcgaca tcttcgacaa ggacggcagc ggctgcatca gcctggatga gtggaaggcc 420
tacqqcaqaa tcaqcqqcat ctgcagcagc gacgaggacg ccgaaaaagac cttcaagcac 480
tgcgacctgg acaacagcgg caagetggac gtggacgaga tgaccagaca gcacctgggc 540
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accetggacg agategtgag cagggecage gacgacatet gegecaaget gggegecace 180
cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240
gactacggca aggaggtgga gttccccgcc ttcgtggacg gctggaagga gctggccaac 300
tacgacetga agetgtggag ceagaacaag aagageetea teagggaetg gggegaggee 360
gtgttcgaca tcttcgacaa ggacggcagc ggcagcatca gcctggatga gtggaaggcc 420
tacggcagaa tcagcggcat ctgcagcagc gacgaggacg ccgaaaagac cttcaagcac 480
tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctgggc 540
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accetggacg agategtgag caaggeeage gaegaeatet gegeeaaget gggegeeaee 180
cccgagcaga ccaagagaca ccgggacgcc gtggaggcct tcttcaagaa gatcggcatg 240
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qtqtttgaca tcttcgacaa ggacggcagc ggcagcatta gcctggatga gtggaaggcc 420
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tgcgacctgg acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctgggc 540
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accetggacg agategtgag caaggecage gacgacatet gegecaaget gggegecace 180
cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240
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tacgacctga agctgtggag ccagaacaat aagagcctca tcagggactg gggcgaggcc 360
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accetggacg agategtgag caaggecage gacgacatet gegecaaget gggegecace 180
cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240
qactacqqca aqqaqqtqqa qttccccqcc ttcgtggacg gctggaagga gctggccaac 300
tacgacctga agctgtggag ccagaacaag aagagcctca tcagggactg gggcgaggcc 360
gtgttcgaca tcttcgacaa ggacggcagc ggcagcatca gcctggatga gtggaaggcc 420
tactgcagaa tcagcggcat ctgcagcagc gacgaggacg ccgaaaagac cttcaagcac 480
tgcqacctqq acaacagcgg caagctggac gtggacgaga tgaccagaca gcacctgggc 540
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accetggacg agategtgag caaggecage gacgaegtet gegecaaget gggegecaee 180
cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240
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tacggcagaa tcagcggcat ctgcagaagc gacgaggacg ccgaaaagac cttcaagcac 480
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accetggacg agategtgag caaggecage gacgacatet gegecagget gggegecace 180
cccgagcaga ccaagagaca ccaggacgcc gtggaggcct tcttcaagaa gatcggcatg 240
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gactacggca aagaggtgga gttccccgcc ttcgtggacg gctggaagga gctggccaac 300
tacgacctqa agctqtgqaq ccaqaacaaq aaqaqcctca tcagggactg gggcgaggcc 360
gtgttcgaca tcttcgacaa ggacggcagc ggcagcatca gcctggatga gtggaaggcc 420
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accetggacg agategtgag caaggecage gacgacatet gegecaaget ggaggecace 180
cccgagcaga ccaagcggca ccaagtgtgc gtggaggcct tcttccgcgg ctgcggcatg 240
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agegagetga agaagtggge eeggaacgag eecaceetga teegegagtg gggegaegee 360
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tgcgacctgg acaacagcgg caagctggac gtggacgaga tgacccggca gcacctgggc 540
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<400> 21
                                                                   33
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